SEQUENCE LISTING

<110> Basi, Guriq
      Saldanha, Jose
      Yednock, Ted

<120> HUMANIZED ANTIBODIES THAT RECOGNIZE
      BETA AMYLOID PEPTIDE

<130> ELN-002

<140> US 10/010,942
<141> 2001-12-06

<150> US 60/251,892
<151> 2000-12-06

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1
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<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(396)

<221> sig_peptide
<222> (1)...(60)

<400> 1

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atg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg    48
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20                 -15                 -10                 -5

gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tcg    96
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
              1               5                   10

gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc   144
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15                  20                  25

ctc tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg   192
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
        30                  35                  40

cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac   240
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 45                  50                  55                  60

tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt   288
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75
```

```
aca ctg aaa atc agc aga ata gag gct gag gat ttg gga ctt tat tat    336
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
            80              85                  90


tgc tgg caa ggt aca cat ttt cct cgg acg ttc ggt gga ggc acc aag    384
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
        95                  100                 105


ctg gaa atc aaa                                                    396
Leu Glu Ile Lys
    110
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<210> 2
<211> 132
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(20)

<400> 2
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Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20             -15             -10                     -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
                1           5               10
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15              20              25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
    30              35              40
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45              50              55                  60
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
                65              70              75
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
            80              85                  90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
        95                  100                 105
Leu Glu Ile Lys
    110
```

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<210> 3
<211> 414
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(414)

<221> sig_peptide
<222> (1)...(57)

<400> 3
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atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt      48
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
            -15                 -10                 -5

gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag      96
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
         1               5                   10

cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc     144
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        15                  20                  25

agt aac tat ggc atg tct tgg gtt cgc cag aat tca gac aag agg ctg     192
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
    30                  35                  40                  45

gag tgg gtt gca tcc att agg agt ggt ggt ggt aga acc tac tat tca     240
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60

gac aat gta aag ggc cga ttc acc atc tcc aga gag aat gcc aag aac     288
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
                65                  70                  75

acc ctg tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg     336
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
            80                  85                  90

tat tat tgt gtc aga tat gat cac tat agt ggt agc tcc gac tac tgg     384
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
        95                  100                 105

ggc cag ggc acc act gtc aca gtc tcc tca                             414
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                 115
```

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<210> 4
<211> 138
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 4
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
            -15                 -10                 -5
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
         1               5                   10
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        15                  20                  25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
30                  35                  40                  45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60
```

```
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
            65              70                  75
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
        80                  85                  90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95                  100                 105
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                 115
```

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<210> 5
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 5
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20             -15             -10                 -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
                1               5               10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
        15                  20                  25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
    30                  35                  40
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45                  50                  55                  60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
        80                  85                  90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105
Val Glu Ile Lys
    110
```

```
<210> 6
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(13)

<400> 6
Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
            -10             -5                  1
Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
    5               10                  15
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
```

```
      20                    -        25           ·             30                    35
Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
                    40                    45                    50
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
                    55                    60                    65
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
                70                    75                    80
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
                85                    90                    95
Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100                    105                    110
```

```
<210> 7
<211> 100
<212> PRT
<213> Homo sapiens
```

```
<400> 7
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
  1                 5                   10                  15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
                20                  25                  30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                  90                  95
Leu Gln Thr Pro
            100
```

```
<210> 8
<211> 138
<212> PRT
<213> Artificial Sequence
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```
<220>
<223> Humanized 3D6 heavy chain variable region
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```
<221> SIGNAL
<222> (1)...(19)
```

```
<400> 8
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
                -15                 -10                 -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
            1                   5                   10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                  20                  25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
```

```
                      65 ·              ·   70                   75
    Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
            80                      85                   90
    Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
        95                     100                   105
    Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    110                  115
```

```
<210> 9
<211> 121
<212> PRT
<213> Homo sapiens

<400> 9
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                   15
Ser ·Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                   30
Ala Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                   45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                   75                   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                   95
Ala Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly
             100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser
            115                 120
```

```
<210> 10
<211> 98
<212> PRT
<213> Homo sapiens

<400> 10
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                   45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                   75                   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                   95
Ala Lys
```

```
<210> 11
<211> 132
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```
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 11
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20              -15                  -10                      -5
Glu Thr Asn Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
                1                5                    10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
            15                  20                  25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
        30                  35                  40
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45                  50                  55                      60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            80                  85                  90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
        95                  100                 105
Val Glu Ile Lys
    110


<210> 12
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 3D6 light chain variable region

<221> SIGNAL
<222> (1)...(19)

<400> 12
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
                -15                 -10                 -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
            1                5                    10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                  20                  25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                      45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                  55                  60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
            65                  70                  75
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
        80                  85                  90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
```

```
          95              .        100      .              105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110                    115
```

```
<210> 13
<211> 393
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(393)

<221> sig_peptide
<222> (1)...(57)

<400> 13
atg aag ttg cct gtt agg ctg ttg gta ctg atg ttc tgg att cct gct    48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
                -15              -10                   -5

tcc agc agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc    96
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
                1            5                   10

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag aac att   144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
        15                  20                  25

ata cat agt aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca   192
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
 30                  35                  40                  45

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct   240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
                50                  55                  60

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca   288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                65                  70                  75

ctc aag atc aag aaa gtg gag gct gag gat ctg gga att tat tac tgc   336
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
            80                  85                  90

ttt caa ggt tca cat gtt ccg ctc acg ttc ggt gct ggg acc aag ctg   384
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
        95                  100                 105

gag ctg gaa                                                        393
Glu Leu Glu
110
```

```
<210> 14
<211> 131
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<212> PRT
<213> Mus·musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 14
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
            -15                 -10                 -5
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
             1               5                   10
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
    15                  20                  25
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
30                  35                  40                  45
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
                50                  55                  60
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                65                  70                  75
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
        80                  85                  90
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
    95                  100                 105
Glu Leu Glu
110


<210> 15
<211> 426
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(426)

<221> sig_peptide
<222> (1)...(57)

<400> 15
atg gac agg ctt act tcc tca ttc ctg ctg ctg att gtc cct gca tat     48
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
            -15                 -10                 -5

gtc ctg tcc cag gct act ctg aaa gag tct ggc cct gga ata ttg cag     96
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
             1               5                   10

tcc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg    144
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
    15                  20                  25

agc act tct ggt atg gga gtg agc tgg att cgt cag cct tca gga aag    192
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
    30                  35                  40                  45
```

```
ggt ctg gag tgg ctg gca cac att tac tgg gat gat gac aag cgc tat    240
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
            50                  55                  60

aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga    288
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
            65                  70                  75

aag cag gta ttc ctc aag atc acc agt gtg gac cct gca gat act gcc    336
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
        80                  85                  90

aca tac tac tgt gtt cga agg ccc att act ccg gta cta gtc gat gct    384
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
        95                 100                 105

atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca            426
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110                 115                 120
```

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<210> 16
<211> 142
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 16
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
            -15                 -10                 -5
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
             1              5                  10
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
    15                  20                  25
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
30                  35                  40                  45
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
            50                  55                  60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
            65                  70                  75
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
        80                  85                  90
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
        95                 100                 105
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110                 115                 120
```

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<210> 17
<211> 136
<212> DNA
<213> Artificial Sequence

<220>
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<223> primer

<400> 17
tccgcaagct tgccgccacc atggacatgc gcgtgcccgc ccagctgctg ggcctgctga 60
tgctgtgggt gtccggctcc tccggctacg tggtgatgac ccagtccccc ctgtccctgc 120
ccgtgacccc cggcga 136

<210> 18
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 18
ctggggggac tggccgggct ctgcagcag ccagttcagg taggtcttgc cgtcggagtc 60
cagcagggac tgggaggact tgcaggagat ggaggcgggc tcgccggggg tcacgggcag 120
ggacaggggg g 131

<210> 19
<211> 146
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
acctgaactg gctgctgcag aagcccggcc agtcccccca gcgcctgatc tacctggtgt 60
ccaagctgga ctccggcgtg cccgaccgct tctccggctc cggctccggc accgacttca 120
ccctgaagat ctcccgcgtg gaggcc 146

<210> 20
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
aattctagga tccactcacg cttgatctcc accttggtgc cctggccgaa ggtgcggggg 60
aagtgggtgc cctgccagca gtagtacacg cccacgtcct cggcctccac gcgggagatc 120
ttcagggtga agtcggtgcc gg 142

<210> 21
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 21
ctggggggac tggccg 16

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<210> 22
<211> 22 .
<212> DNA
<<213> Artificial Sequence

<220>
<223> primer

<400> 22
acctgaactg gctgctgcag aa                                          22

<210> 23
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 23
acagaaagct tgccgccacc atggagtttg ggctgagctg gctttttctt gtggctattt 60
taaaaggtgt ccagtgtgag gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg 120
gcggctccct gcgcctgt                                              138

<210> 24
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 24
gccgccggag cggatggagg ccacccactc caggcccttg ccggggggcct ggcgcaccca 60
ggacatgccg tagttggaga aggtgaagcc ggaggcggcg caggacaggc gcagggagcc 120
gccgggctgc accag                                                135

<210> 25
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
ctggagtggg tggcctccat ccgctccggc ggcggccgca cctactactc cgacaacgtg 60
aagggccgct tcaccatctc ccgcgacaac gccaagaact ccctgtacct gcagatgaac 120
tccctgcgcg ccgaggacac cg                                        142

<210> 26
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> primer
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<400> 26
ctgcaaggat ccactcaccg gaggacacgg tcaccagggt gccctggccc cagtagtcgg 60
aggagccgga gtagtggtcg tagcgcacgc agtagtacag ggcggtgtcc tcggcgcgca 120
gggagttcat ctgcaggtac aggg   144

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27
gccgccggag cggatg   16

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 28
ctggagtggg tggcctccat   20

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
tccgcaagct tgccgccac   19

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
aattctagga tccactcacg cttgatctc   29

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 31
acagaaagct tgccgccacc atg   23

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
ctgcaaggat ccactcaccg ga   22

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> native ABeta peptide

<400> 33
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
 1   5   10

<210> 34
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 1 VL

<400> 34
atggacatgc gcgtgcccgc ccagctgctg ggcctgctga tgctgtgggt gtccggctcc 60
tccggctacg tggtgatgac ccagtccccc ctgtccctgc ccgtgacccc cggcgagccc 120
gcctccatct cctgcaagtc ctcccagtcc ctgctggact ccgacggcaa gacctacctg 180
aactggctgc tgcagaagcc cggccagtcc ccccagcgcc tgatctacct ggtgtccaag 240
ctggactccg gcgtgcccga ccgcttctcc ggctccggct ccggcaccga cttcaccctg 300
aagatctccc gcgtggaggc cgaggacgtg ggcgtgtact actgctggca gggcacccac 360
ttcccccgca ccttcggcca gggcaccaag gtggagatca ag   402

<210> 35
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 2 VL

<400> 35
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tccggcgacg tggtgatgac ccagtccccc ctgtccctgc ccgtgacccc cggcgagccc 120
gcctccatct cctgcaagtc ctcccagtcc ctgctggact ccgacggcaa gacctacctg 180

```
aactggctgc tgcagaagcc cggccagtcc ccccagcgcc tgatctacct ggtgtccaag 240
ctggactccg gcgtgcccga ccgcttctcc ggctccggct ccggcaccga cttcaccctg 300
aagatctccc gcgtggaggc cgaggacgtg ggcgtgtact actgctggca gggcacccac 360
ttccccgca  ccttcggcca gggcaccaag gtggagatca ag                    402
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<210> 36
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 1 VH

<400> 36
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gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg gcggctccct gcgcctgtcc 120
tgcgccgcct ccggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggcccc 180
ggcaagggcc tggagtgggt ggcctccatc cgctccggcg gcggccgcac ctactactcc 240
gacaacgtga agggccgctt caccatctcc cgcgacaacg ccaagaactc cctgtacctg 300
cagatgaact ccctgcgcgc cgaggacacc gccctgtact actgcgtgcg ctacgaccac 360
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<210> 37
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 2 VH

<400> 37
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tgcgccgcct ccggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggcccc 180
ggcaagggcc tggagtgggt ggcctccatc cgctccggcg gcggccgcac ctactactcc 240
gacaacgtga agggccgctt caccatctcc cgcgacaact ccaagaacac cctgtacctg 300
cagatgaact ccctgcgcgc cgaggacacc gccgtgtact actgcgtgcg ctacgaccac 360
tactccggct cctccgacta ctggggccag ggcaccctgg tgaccgtgtc ctcc      414
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<210> 38
<211> 770
<212> PRT
<213> Homo sapiens

<400> 38
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Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1           5                  10                  15
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
            20              25                  30
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
        35                  40                  45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
    50                  55                  60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65                  70                  75                  80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
                85                  90                  95
```

```
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
        100                 105                 110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
        115                 120                 125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
    130                 135                 140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145                 150                 155                 160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
                165                 170                 175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
            180                 185                 190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
        195                 200                 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
    210                 215                 220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225                 230                 235                 240
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
            245                 250                 255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
            260                 265                 270
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
        275                 280                 285
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
    290                 295                 300
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305                 310                 315                 320
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
            325                 330                 335
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
            340                 345                 350
Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
        355                 360                 365
Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
    370                 375                 380
Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385                 390                 395                 400
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
            405                 410                 415
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
            420                 425                 430
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
        435                 440                 445
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
    450                 455                 460
Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465                 470                 475                 480
Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
            485                 490                 495
Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
            500                 505                 510
Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
        515                 520                 525
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
    530                 535                 540
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
```

```
     545              .        550          .         555                 560
     Glu  Val  Asp  Glu  Leu  Leu  Gln  Lys  Glu  Gln  Asn  Tyr  Ser  Asp  Asp  Val
                          565                     570                     575
     Leu  Ala  Asn  Met  Ile  Ser  Glu  Pro  Arg  Ile  Ser  Tyr  Gly  Asn  Asp  Ala
                          580                     585                     590
     Leu  Met  Pro  Ser  Leu  Thr  Glu  Thr  Lys  Thr  Thr  Val  Glu  Leu  Leu  Pro
                     595                     600                     605
     Val  Asn  Gly  Glu  Phe  Ser  Leu  Asp  Asp  Leu  Gln  Pro  Trp  His  Ser  Phe
                610                     615                     620
     Gly  Ala  Asp  Ser  Val  Pro  Ala  Asn  Thr  Glu  Asn  Glu  Val  Glu  Pro  Val
     625                     630                     635                     640
     Asp  Ala  Arg  Pro  Ala  Ala  Asp  Arg  Gly  Leu  Thr  Thr  Arg  Pro  Gly  Ser
                          645                     650                     655
     Gly  Leu  Thr  Asn  Ile  Lys  Thr  Glu  Glu  Ile  Ser  Glu  Val  Lys  Met  Asp
                     660                     665                     670
     Ala  Glu  Phe  Arg  His  Asp  Ser  Gly  Tyr  Glu  Val  His  His  Gln  Lys  Leu
                675                     680                     685
     Val  Phe  Phe  Ala  Glu  Asp  Val  Gly  Ser  Asn  Lys  Gly  Ala  Ile  Ile  Gly
                690                     695                     700
     Leu  Met  Val  Gly  Gly  Val  Val  Ile  Ala  Thr  Val  Ile  Val  Ile  Thr  Leu
     705                     710                     715                     720
     Val  Met  Leu  Lys  Lys  Lys  Gln  Tyr  Thr  Ser  Ile  His  His  Gly  Val  Val
                          725                     730                     735
     Glu  Val  Asp  Ala  Ala  Val  Thr  Pro  Glu  Glu  Arg  His  Leu  Ser  Lys  Met
                     740                     745                     750
     Gln  Gln  Asn  Gly  Tyr  Glu  Asn  Pro  Thr  Tyr  Lys  Phe  Phe  Glu  Gln  Met
                     755                     760                     765
     Gln  Asn
          770
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<210> 39
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 39
actagtcgac atgaagttgc ctgttaggct gttggtgctg                    40

<210> 40
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 40
actagtcgac atggagwcag acacactcct gytatgggt                     39

<210> 41
<211> 40
<212> DNA
<213> Artificial Sequence
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<220>
<223> primer

<400> 41
actagtcgac atgagtgtgc tcactcaggt cctggsgttg                    40

<210> 42
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 42
actagtcgac atgaggrccc ctgctcagwt tyttggmwtc ttg                43

<210> 43
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
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<400> 43
actagtcgac atggatttwc aggtgcagat twtcagcttc                    40

<210> 44
<211> 37
<212> DNA
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<220>
<223> primer

<400> 44
actagtcgac atgaggtkcy ytgytsagyt yctgrgg                       37

<210> 45
<211> 41
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<220>
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<400> 45
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<210> 46
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<212> DNA
<213> Artificial Sequence

<220>
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<223> primer

<400> 46
actagtcgac atgtggggay ctktttycmm tttttcaatt g   41

<210> 47
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<212> DNA
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<220>
<223> primer

<400> 47
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<210> 48
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<220>
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<400> 48
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<210> 49
<211> 38
<212> DNA
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<220>
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<400> 49
actagtcgac atggaagccc cagctcagct tctcttcc   38

<210> 50
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<220>
<223> primer

<400> 50
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<210> 51
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

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<400> 51
actagtcgac atgaaatgca gctgggtcat sttcttc                    37

<210> 52
<211> 36
<212> DNA
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<220>
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<400> 52
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<210> 53
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<220>
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<400> 53
actagtcgac atgaagwtgt ggttaaactg ggttttt                    37

<210> 54
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<212> DNA
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<220>
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<400> 54
actagtcgac atgractttg ggytcagctt grttt                      35

<210> 55
<211> 40
<212> DNA
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<220>
<223> primer

<400> 55
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<210> 56
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<220>
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<400> 56
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<210> 57
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 57
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<210> 58
<211> 33
<212> DNA
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<220>
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<400> 58
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<210> 59
<211> 40
<212> DNA
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<220>
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<400> 59
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<210> 60
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<220>
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<400> 60
actagtcgac atgggcagac ttacattctc attcctg                   37

<210> 61
<211> 38
<212> DNA
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<220>
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<400> 61
actagtcgac atggattttg ggctgatttt ttttattg                  38

<210> 62
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<211> 37
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<220>
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actagtcgac atgatggtgt taagtcttct gtacctg   37

<210> 63
<211> 27
<212> DNA
<213> Artificial Sequence

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<400> 63
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